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STANDAGE, SCOTT

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ANTIBIOTIC C-1027

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D8
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D8
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 <210> 77
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 <210> 78
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 <210> 79
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D8
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 tcagccgcgc gccgacgg 18
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D8
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gtgaccacga acaccatc 18

<210> 98
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<210> 99
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18

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27

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18

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26

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22

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DS
Cont

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<223> sgcA gene

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<223> sgcB gene

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aactgacgaa gcgtcatcgc cgtgacaagg aggcggaccg atg agg atg ctg gtg 115
Met Arg Met Leu Val
1 5

acg ggc gga gcg ggt ttc atc ggc tcg cag ttc gtg cgg gcc aca ctg 163
Thr Gly Gly Ala Gly Phe Ile Gly Ser Gln Phe Val Arg Ala Thr Leu
10 15 20

cac ggc gag ctg ccg ggt tcc gag gac gcc cgg gtg acg gtc ctg gac 211
His Gly Glu Leu Pro Gly Ser Glu Asp Ala Arg Val Thr Val Leu Asp
25 30 35

aag ctg acg tac tcc ggc aat ccg gcc aac ctc acc tcc gtc gcg gcc 259
Lys Leu Thr Tyr Ser Gly Asn Pro Ala Asn Leu Thr Ser Val Ala Ala
40 45 50

cat ccg cgg tac acc ttc gtc cag ggc gac acc gtc gac ccg cgc gtc 307
His Pro Arg Tyr Thr Phe Val Gln Gly Asp Thr Val Asp Pro Arg Val
55 60 65

gtc gac gag gtg gtc gcc ggc cac gac gtc atc gtc cac ttc gcg gcg 355
Val Asp Glu Val Val Ala Gly His Asp Val Ile Val His Phe Ala Ala
70 75 80 85

gag tcg cac gtg gac cgc tcg atc gac acc gcc acc cgg ttc gtc acg 403
Glu Ser His Val Asp Arg Ser Ile Asp Thr Ala Thr Arg Phe Val Thr
90 95 100

acc aac gtg ctc ggg acc cag acg ctg ctg gaa gcg gct ctc cgg cac 451

Thr Asn Val Leu Gly Thr Gln Thr Leu Leu Glu Ala Ala Leu Arg His
 105 110 115
 ggg gtc ggc cgg ttc gtg cac gtg tcg acc gac gag gtc tac ggg tcg 499
 Gly Val Gly Arg Phe Val His Val Ser Thr Asp Glu Val Tyr Gly Ser
 120 125 130
 atc gcc tcc ggc tca tgg acc gag gac acc ccg ctc gcc ccc aac gtc 547
 Ile Ala Ser Gly Ser Trp Thr Glu Asp Thr Pro Leu Ala Pro Asn Val
 135 140 145
 ccc tac gcg gcg tcg aag gcg ggt tcg gac ctg atg gcg ctc gcc tgg 595
 Pro Tyr Ala Ala Ser Lys Ala Gly Ser Asp Leu Met Ala Leu Ala Trp
 150 155 160 165
 cac cgc acc cgg ggc ctg gac gtc gtc gtc acc cgg tgc acc aac aac 643
 His Arg Thr Arg Gly Leu Asp Val Val Val Thr Arg Cys Thr Asn Asn
 170 175 180
 tac ggt ccc tac cag tac ccc gag aag gtg atc ccg ctc ttc gtc acc 691
 Tyr Gly Pro Tyr Gln Tyr Pro Glu Lys Val Ile Pro Leu Phe Val Thr
 185 190 195
 aac atc ctc gac ggc ttg cgg gtg ccc ctg tac ggg gac ggc gcc cac 739
 Asn Ile Leu Asp Gly Leu Arg Val Pro Leu Tyr Gly Asp Gly Ala His
 200 205 210
 cgc cgg gac tgg ctg cac gtg tcc gac cac tgc cgg gcc atc cag atg 787
 Arg Arg Asp Trp Leu His Val Ser Asp His Cys Arg Ala Ile Gln Met
 215 220 225
 gtc atg aac tcc ggc cgg gcc ggg gag gtc tac cac atc ggc ggc gcc 835
 Val Met Asn Ser Gly Arg Ala Gly Glu Val Tyr His Ile Gly Gly Gly
 230 235 240 245
 acc gaa ctc tcc aac gag gaa ctc acc ggc ctg ttg ctc acg gcg tgc 883
 Thr Glu Leu Ser Asn Glu Glu Leu Thr Gly Leu Leu Leu Thr Ala Cys
 250 255 260
 ggc acc gac tgg tcc tgc gtg gac cgg gtg gcc gac cgg cag ggg cac 931
 Gly Thr Asp Trp Ser Cys Val Asp Arg Val Ala Asp Arg Gln Gly His
 265 270 275
 gac cgc cgc tac tcg ctc gac atc acg aag atc cgg cag gaa ctg ggc 979
 Asp Arg Arg Tyr Ser Leu Asp Ile Thr Lys Ile Arg Gln Glu Leu Gly
 280 285 290
 tac gag ccc ctg gtc gcc ttc gag gac ggc ctg gcc gcg acg gtg aag 1027
 Tyr Glu Pro Leu Val Ala Phe Glu Asp Gly Leu Ala Ala Thr Val Lys
 295 300 305
 tgg tac cac gag aac cgt tcg tgg tgg cag ccg ctg aag gaa gcg gcc 1075
 Trp Tyr His Glu Asn Arg Ser Trp Trp Gln Pro Leu Lys Glu Ala Ala
 310 315 320 325
 ggc ctc ctg gac gcc gtc ggc tgacggcagc caccgctagg aacacccccag 1126
 Gly Leu Leu Asp Ala Val Gly
 330
 gaaaggagcc acctcc gtg aca gca gtc aag gag ccg acg tcc cgc gca gga 1178
 Met Thr Ala Val Lys Glu Pro Thr Ser Arg Ala Gly
 335 340
 cgg cgg gag tgg atc gct ctc gtc gtc ctc tcc ttg ccc acg atg ctg 1226

D8
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Arg 345	Arg	Glu	Trp	Ile	Ala 350	Leu	Val	Val	Leu	Ser 355	Leu	Pro	Thr	Met	Leu 360	
ttg	atg	ctg	gac	atc	aac	gtc	ctc	atg	ctg	gcc	ttg	ccg	cag	ttg	agc	1274
Leu	Met	Leu	Asp	Ile 365	Asn	Val	Leu	Met	Leu 370	Ala	Leu	Pro	Gln	Leu 375	Ser	
gag	gat	ctc	ggc	gcg	agc	agc	acg	caa	cag	ctg	tgg	atc	acc	gac	atc	1322
Glu	Asp	Leu	Gly 380	Ala	Ser	Ser	Thr	Gln 385	Leu	Trp	Ile	Thr 390	Asp	Ile		
tac	gga	ttc	gcg	atc	gcc	ggc	ttc	ctg	gtg	acc	atg	ggc	acc	ctc	ggc	1370
Tyr	Gly	Phe 395	Ala	Ile	Ala	Gly	Phe 400	Leu	Val	Thr	Met	Gly 405	Thr	Leu	Gly	
gac	cgg	atc	ggc	cgc	cgc	agg	ctc	ctg	ctc	ggg	ggc	gcg	gcc	gtc	ttc	1418
Asp	Arg 410	Ile	Gly	Arg	Arg	Arg 415	Leu	Leu	Leu	Gly 420	Gly	Ala	Ala	Val	Phe	
gcg	gtc	gtg	tcc	gtc	gtc	gcc	gcg	ttc	tcc	gac	agc	gcg	gcg	atg	ctc	1466
Ala	Val	Val	Ser	Val	Val 430	Ala	Ala	Phe	Ser	Asp 435	Ser	Ala	Ala	Met	Leu 440	
gtc	gtc	agc	cgc	gcc	gtg	ctc	ggc	gtc	gcc	ggg	gcc	acg	gtg	atg	ccc	1514
Val	Val	Ser	Arg	Ala 445	Val	Leu	Gly	Val	Ala 450	Gly	Ala	Thr	Val	Met 455	Pro	
tcg	acg	ctc	gcg	ctc	atc	agc	aac	atg	ttc	gag	gac	ccc	aag	gag	cgg	1562
Ser	Thr	Leu	Ala 460	Leu	Ile	Ser	Asn 465	Met	Phe	Glu	Asp	Pro	Lys 470	Glu	Arg	
ggc	acc	gcc	atc	gcc	atg	tgg	gcg	agc	gcc	atg	atg	gcc	gga	gtc	gcc	1610
Gly	Thr	Ala 475	Ile	Ala	Met	Trp	Ala 480	Ser	Ala	Met	Met	Ala 485	Gly	Val	Ala	
ctc	ggg	ccc	gcc	gtc	ggc	ggc	ctg	gtc	ctc	gcc	gcg	ttc	tgg	tgg	gga	1658
Leu	Gly 490	Pro	Ala	Val	Gly 495	Gly	Leu	Val	Leu	Ala 500	Ala	Phe	Trp	Trp	Gly	
tcg	gtg	ttc	ctc	atc	gcc	gtt	ccg	gtg	atg	ctg	ctg	gtg	gtg	gtc	acc	1706
Ser	Val	Phe	Leu	Ile 510	Ala	Val	Pro	Val	Met	Leu 515	Leu	Val	Val	Val	Thr 520	
ggc	ccc	gtg	ctg	ctc	acc	gag	tcc	cgc	gac	ccg	gac	gcc	gga	cgg	ctg	1754
Gly	Pro	Val	Leu 525	Leu	Thr	Glu	Ser	Arg	Asp 530	Pro	Asp	Ala	Gly	Arg 535	Leu	
gac	ctg	ctg	agc	gcg	ggg	ctc	tcc	ctc	gcg	acc	gtg	ctg	ccg	gtg	atc	1802
Asp	Leu	Leu	Ser 540	Ala	Gly	Leu	Ser	Leu 545	Ala	Thr	Val	Leu 550	Pro	Val	Ile	
tac	gga	ctg	aag	gag	ctg	gcc	cgg	acc	ggg	tgg	gac	ccg	ctc	gcc	gcc	1850
Tyr	Gly	Leu 555	Lys	Glu	Leu	Ala	Arg 560	Thr	Gly	Trp	Asp	Pro 565	Leu	Ala	Ala	
ggc	gcg	gtg	gtc	ctc	ggc	gtg	atc	ttc	ggc	gcg	ctg	ttc	gtc	cag	cgc	1898
Gly	Ala	Val	Val	Leu	Gly 570	Val	Ile 575	Phe	Gly	Ala 580	Leu	Phe	Val	Gln	Arg	
cag	cgg	cgg	ttg	gcc	gac	ccc	atg	ctg	gac	ctc	ggc	ctc	ttc	gcc	gac	1946
Gln	Arg	Arg	Leu	Ala 585	Asp 590	Pro	Met	Leu	Asp 595	Leu	Gly	Leu	Phe	Ala 600	Asp	

DS
Cont

cgc acc ctg cgg gcg ggt ctg acg gtc agt ctg gtc aac gcc gtc atc	1994
Arg Thr Leu Arg Ala Gly Leu Thr Val Ser Leu Val Asn Ala Val Ile	
605 610 615	
atg ggc ggg acc gga ctg atg gtc gcc ctg tac ctc cag acg atc gcc	2042
Met Gly Gly Thr Gly Leu Met Val Ala Leu Tyr Leu Gln Thr Ile Ala	
620 625 630	
ggt cac tcc ccg ttg gcc gcc ggg ctg tgg ctg ctg atc ccg gcc tgc	2090
Gly His Ser Pro Leu Ala Ala Gly Leu Trp Leu Leu Ile Pro Ala Cys	
635 640 645	
atg ctc gtc gtg ggc gta cag ctg tgc aac ctg ctg gcc cag cgg atg	2138
Met Leu Val Val Gly Val Gln Leu Ser Asn Leu Ala Gln Arg Met	
650 655 660	
ccc cct tcc cgg gtg ctg ctg ggg gga ctg ctg atc gcg gcc gtc gga	2186
Pro Pro Ser Arg Val Leu Leu Gly Gly Leu Leu Ile Ala Ala Val Gly	
665 670 675 680	
cag ctc ctg atc acc cag gtg gac acc gag gac acc gcc ctc ctc atc	2234
Gln Leu Leu Ile Thr Gln Val Asp Thr Glu Asp Thr Ala Leu Leu Ile	
685 690 695	
gcg gcc acc acc ctg atc tac ttc ggc gcc tca ccg gtg ggg ccg atc	2282
Ala Ala Thr Thr Leu Ile Tyr Phe Gly Ala Ser Pro Val Gly Pro Ile	
700 705 710	
acc acg ggc gcg atc atg gga gcc gcg ccc ccg gag aag gcg ggt gcc	2330
Thr Thr Gly Ala Ile Met Gly Ala Ala Pro Pro Glu Lys Ala Gly Ala	
715 720 725	
gcc tgc tgc ctg tcc gcc acc ggc ggc gag ttc gga gtg gcg ctc ggc	2378
Ala Ser Ser Leu Ser Ala Thr Gly Gly Glu Phe Gly Val Ala Leu Gly	
730 735 740	
atc gcg ggc ctg ggg agt ctg ggc acc gtc gtg tac agc gcc ggg gtc	2426
Ile Ala Gly Leu Gly Ser Leu Gly Thr Val Tyr Ser Ala Gly Val	
745 750 755 760	
gag gtg ccg gac gcg gcc ggg ccc gcc gac gcc gac gcc gcg cag gag	2474
Glu Val Pro Asp Ala Ala Gly Pro Ala Asp Ala Asp Ala Ala Gln Glu	
765 770 775	
agc atc gcc ggc gcc ctg cac acg gcc ggt cag ctg gca ccg ggc agc	2522
Ser Ile Ala Gly Ala Leu His Thr Ala Gly Gln Leu Ala Pro Gly Ser	
780 785 790	
gcc gac gcc ctg ctg gac tcc gcg cgc gcg gcc ttc acc agc ggc gtg	2570
Ala Asp Ala Leu Leu Asp Ser Ala Arg Ala Ala Phe Thr Ser Gly Val	
795 800 805	
cag tcc gtc gcc gcc gtc tgc gcc gtg ttc tcc ctg gcg ctc gcc gtc	2618
Gln Ser Val Ala Ala Val Cys Ala Val Phe Ser Leu Ala Leu Ala Val	
810 815 820	
ctc atc ggc acc cgg ctg cgg gac att tcc gcg atg gac cac ggg cac	2666
Leu Ile Gly Thr Arg Leu Arg Asp Ile Ser Ala Met Asp His Gly His	
825 830 835 840	
ggc gag gaa ccg gcc gag aac gac gct caa ccg gcc aca tgagcgcact	2715
Gly Glu Glu Pro Ala Glu Asn Asp Ala Gln Pro Ala Thr	
845 850	

DS
Cont.

tccggagatg caacggccgc cgtcgaggta tgaggatcac cttccgggggt gcacctgcac 2775
 ggcaacggag gcgtagtgga gtactggaac agcacggcgg agaccatgcc ccgccaggaa 2835
 ctccaacagt ggaagtggcg caggctccag gccgccatgg accacgccag aaggctttcg 2895
 cccttctggc gggaacgact ccccgagaac atcacctcca tggcgggacta cgcgggcgcg 2955
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 <212> PRT
 <213> Streptomyces globisporus

<220>
 <223> sgcA

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 Val Thr Val Leu Asp Lys Leu Thr Tyr Ser Gly Asn Pro Ala Asn Leu
 35 40 45
 Thr Ser Val Ala Ala His Pro Arg Tyr Thr Phe Val Gln Gly Asp Thr
 50 55 60
 Val Asp Pro Arg Val Val Asp Glu Val Val Ala Gly His Asp Val Ile
 65 70 75 80
 Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Asp Thr Ala
 85 90 95
 Thr Arg Phe Val Thr Thr Asn Val Leu Gly Thr Gln Thr Leu Leu Glu
 100 105 110
 Ala Ala Leu Arg His Gly Val Gly Arg Phe Val His Val Ser Thr Asp
 115 120 125
 Glu Val Tyr Gly Ser Ile Ala Ser Gly Ser Trp Thr Glu Asp Thr Pro
 130 135 140
 Leu Ala Pro Asn Val Pro Tyr Ala Ala Ser Lys Ala Gly Ser Asp Leu
 145 150 155 160
 Met Ala Leu Ala Trp His Arg Thr Arg Gly Leu Asp Val Val Val Thr
 165 170 175
 Arg Cys Thr Asn Asn Tyr Gly Pro Tyr Gln Tyr Pro Glu Lys Val Ile
 180 185 190
 Pro Leu Phe Val Thr Asn Ile Leu Asp Gly Leu Arg Val Pro Leu Tyr
 195 200 205
 Gly Asp Gly Ala His Arg Arg Asp Trp Leu His Val Ser Asp His Cys
 210 215 220

DB
Cont

Arg Ala Ile Gln Met Val Met Asn Ser Gly Arg Ala Gly Glu Val Tyr
 225 230 235 240
 His Ile Gly Gly Gly Thr Glu Leu Ser Asn Glu Glu Leu Thr Gly Leu
 245 250 255
 Leu Leu Thr Ala Cys Gly Thr Asp Trp Ser Cys Val Asp Arg Val Ala
 260 265 270
 Asp Arg Gln Gly His Asp Arg Arg Tyr Ser Leu Asp Ile Thr Lys Ile
 275 280 285
 Arg Gln Glu Leu Gly Tyr Glu Pro Leu Val Ala Phe Glu Asp Gly Leu
 290 295 300
 Ala Ala Thr Val Lys Trp Tyr His Glu Asn Arg Ser Trp Trp Gln Pro
 305 310 315 320
 Leu Lys Glu Ala Ala Gly Leu Leu Asp Ala Val Gly
 325 330

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<220>
 <223> sgcB

<400> 114
 Met Thr Ala Val Lys Glu Pro Thr Ser Arg Ala Gly Arg Arg Glu Trp
 1 5 10 15
 Ile Ala Leu Val Val Leu Ser Leu Pro Thr Met Leu Leu Met Leu Asp
 20 25 30
 Ile Asn Val Leu Met Leu Ala Leu Pro Gln Leu Ser Glu Asp Leu Gly
 35 40 45
 Ala Ser Ser Thr Gln Gln Leu Trp Ile Thr Asp Ile Tyr Gly Phe Ala
 50 55 60
 Ile Ala Gly Phe Leu Val Thr Met Gly Thr Leu Gly Asp Arg Ile Gly
 65 70 75 80
 Arg Arg Arg Leu Leu Leu Gly Gly Ala Ala Val Phe Ala Val Val Ser
 85 90 95
 Val Val Ala Ala Phe Ser Asp Ser Ala Ala Met Leu Val Val Ser Arg
 100 105 110
 Ala Val Leu Gly Val Ala Gly Ala Thr Val Met Pro Ser Thr Leu Ala
 115 120 125
 Leu Ile Ser Asn Met Phe Glu Asp Pro Lys Glu Arg Gly Thr Ala Ile
 130 135 140
 Ala Met Trp Ala Ser Ala Met Met Ala Gly Val Ala Leu Gly Pro Ala
 145 150 155 160
 Val Gly Gly Leu Val Leu Ala Ala Phe Trp Trp Gly Ser Val Phe Leu
 165 170 175

D8
 Cont.

Ile Ala Val Pro Val Met Leu Leu Val Val Val Thr Gly Pro Val Leu
 180 185 190
 Leu Thr Glu Ser Arg Asp Pro Asp Ala Gly Arg Leu Asp Leu Leu Ser
 195 200 205
 Ala Gly Leu Ser Leu Ala Thr Val Leu Pro Val Ile Tyr Gly Leu Lys
 210 215 220
 Glu Leu Ala Arg Thr Gly Trp Asp Pro Leu Ala Ala Gly Ala Val Val
 225 230 235 240
 Leu Gly Val Ile Phe Gly Ala Leu Phe Val Gln Arg Gln Arg Arg Leu
 245 250 255
 Ala Asp Pro Met Leu Asp Leu Gly Leu Phe Ala Asp Arg Thr Leu Arg
 260 265 270
 Ala Gly Leu Thr Val Ser Leu Val Asn Ala Val Ile Met Gly Gly Thr
 275 280 285
 Gly Leu Met Val Ala Leu Tyr Leu Gln Thr Ile Ala Gly His Ser Pro
 290 295 300
 Leu Ala Ala Gly Leu Trp Leu Leu Ile Pro Ala Cys Met Leu Val Val
 305 310 315 320
 Gly Val Gln Leu Ser Asn Leu Leu Ala Gln Arg Met Pro Pro Ser Arg
 325 330 335
 Val Leu Leu Gly Gly Leu Leu Ile Ala Ala Val Gly Gln Leu Leu Ile
 340 345 350
 Thr Gln Val Asp Thr Glu Asp Thr Ala Leu Leu Ile Ala Ala Thr Thr
 355 360 365
 Leu Ile Tyr Phe Gly Ala Ser Pro Val Gly Pro Ile Thr Thr Gly Ala
 370 375 380
 Ile Met Gly Ala Ala Pro Pro Glu Lys Ala Gly Ala Ala Ser Ser Leu
 385 390 395 400
 Ser Ala Thr Gly Gly Glu Phe Gly Val Ala Leu Gly Ile Ala Gly Leu
 405 410 415
 Gly Ser Leu Gly Thr Val Val Tyr Ser Ala Gly Val Glu Val Pro Asp
 420 425 430
 Ala Ala Gly Pro Ala Asp Ala Asp Ala Ala Gln Glu Ser Ile Ala Gly
 435 440 445
 Ala Leu His Thr Ala Gly Gln Leu Ala Pro Gly Ser Ala Asp Ala Leu
 450 455 460
 Leu Asp Ser Ala Arg Ala Ala Phe Thr Ser Gly Val Gln Ser Val Ala
 465 470 475 480
 Ala Val Cys Ala Val Phe Ser Leu Ala Leu Ala Val Leu Ile Gly Thr
 485 490 495
 Arg Leu Arg Asp Ile Ser Ala Met Asp His Gly His Gly Glu Glu Pro
 500 505 510

D8
 Cont.

Ala Glu Asn Asp Ala Gln Pro Ala Thr
515 520

<210> 115

<211> 329

<212> PRT

<213> Saccharopolyspora erythraea

<400> 115

Met Arg Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Tyr
1 5 10 15

Val Arg Gln Leu Leu Gly Gly Ala Tyr Pro Ala Phe Ala Gly Ala Asp
20 25 30

Val Val Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Glu Glu Asn Leu
35 40 45

Arg Pro Val Ala Asp Asp Pro Arg Phe Arg Phe Val Arg Gly Asp Ile
50 55 60

Cys Glu Trp Asp Val Val Ser Glu Val Met Arg Glu Val Asp Val Val
65 70 75 80

Val His Phe Ala Ala Glu Thr His Val Asp Arg Ser Ile Leu Gly Ala
85 90 95

Ser Asp Phe Val Val Thr Asn Val Val Gly Thr Asn Thr Leu Leu Gln
100 105 110

Gly Ala Leu Ala Ala Asn Val Ser Lys Phe Val His Val Ser Thr Asp
115 120 125

Glu Val Tyr Gly Thr Ile Glu His Gly Ser Trp Pro Glu Asp His Leu
130 135 140

Leu Glu Pro Asn Ser Pro Tyr Ser Ala Ala Lys Ala Gly Ser Asp Leu
145 150 155 160

Ile Ala Arg Ala Tyr His Arg Thr His Gly Leu Pro Val Cys Ile Thr
165 170 175

Arg Cys Ser Asn Asn Tyr Gly Pro Tyr Gln Phe Pro Glu Lys Val Leu
180 185 190

Pro Leu Phe Ile Thr Asn Leu Met Asp Gly Arg Arg Val Pro Leu Tyr
195 200 205

Gly Asp Gly Leu Asn Val Arg Asp Trp Leu His Val Thr Asp His Cys
210 215 220

Arg Gly Ile Gln Leu Val Ala Glu Ser Gly Arg Ala Gly Glu Ile Tyr
225 230 235 240

Asn Ile Gly Gly Gly Thr Glu Leu Thr Asn Lys Glu Leu Thr Glu Arg
245 250 255

Val Leu Glu Leu Met Gly Gln Asp Trp Ser Met Val Gln Pro Val Thr
260 265 270

Asp Arg Lys Gly His Asp Arg Arg Tyr Ser Val Asp His Thr Lys Ile
275 280 285

D8
Cont.

Ser Glu Glu Leu Gly Tyr Glu Pro Val Val Pro Phe Glu Arg Gly Leu
290 295 300

Ala Glu Thr Ile Glu Trp Tyr Arg Asp Asn Arg Ala Trp Trp Glu Pro
305 310 315 320

Leu Lys Ser Ala Pro Asp Gly Gly Lys
325

<210> 116

<211> 333

<212> PRT

<213> Streptomyces fradiae

<400> 116

Met Arg Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Phe
1 5 10 15

Thr Gly Gln Leu Leu Thr Gly Ala Tyr Pro Asp Leu Gly Ala Thr Arg
20 25 30

Thr Val Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Pro Ala Asn Leu
35 40 45

Glu His Val Ala Gly His Pro Asp Leu Glu Phe Val Arg Gly Asp Ile
50 55 60

Ala Asp His Gly Trp Trp Arg Arg Leu Met Glu Gly Val Gly Leu Val
65 70 75 80

Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Glu Ser Ser
85 90 95

Glu Ala Phe Val Arg Thr Asn Val Glu Gly Thr Arg Val Leu Leu Gln
100 105 110

Ala Ala Val Asp Ala Gly Val Gly Arg Phe Val His Ile Ser Thr Asp
115 120 125

Glu Val Tyr Gly Ser Ile Ala Glu Gly Ser Trp Pro Glu Asp His Pro
130 135 140

Val Ala Pro Asn Ser Pro Tyr Ala Ala Thr Lys Lys Ala Ser Asp Leu
145 150 155 160

Leu Ala Leu Ala Tyr His Arg Thr Tyr Gly Leu Asp Val Arg Val Thr
165 170 175

Arg Cys Ser Asn Asn Tyr Gly Pro Arg Gln Tyr Pro Glu Lys Ala Val
180 185 190

Pro Leu Phe Thr Thr Asn Leu Leu Asp Gly Leu Pro Val Pro Leu Tyr
195 200 205

Gly Asp Gly Gly Asn Thr Arg Glu Trp Leu His Val Asp Asp His Cys
210 215 220

Arg Gly Val Ala Leu Val Gly Ala Gly Gly Arg Pro Gly Val Ile Tyr
225 230 235 240

Asn Ile Gly Gly Gly Thr Glu Leu Thr Asn Ala Glu Leu Thr Asp Arg
245 250 255

D8
Cont

Ile Leu Glu Leu Cys Gly Ala Asp Arg Ser Ala Leu Arg Arg Val Ala
260 265 270
Asp Arg Pro Gly His Asp Arg Arg Tyr Ser Val Asp Thr Thr Lys Ile
275 280 285
Arg Glu Glu Leu Gly Tyr Ala Pro Arg Thr Gly Ile Thr Glu Gly Leu
290 295 300
Ala Gly Thr Val Ala Trp Tyr Arg Asp Asn Arg Ala Trp Trp Glu Pro
305 310 315 320
Leu Lys Arg Ser Pro Gly Gly Arg Glu Leu Glu Arg Ala
325 330

<210> 117
<211> 331
<212> PRT
<213> Streptomyces argillaceus

<400> 117
Met Thr Thr Thr Ser Ile Leu Val Thr Gly Gly Ala Gly Phe Ile Gly
1 5 10 15
Ser His Tyr Val Arg Thr Leu Leu Gly Pro Arg Gly Val Pro Asp Val
20 25 30
Thr Val Thr Val Leu Asp Lys Leu Thr Tyr Ala Gly Thr Leu Thr Asn
35 40 45
Leu Ala Glu Val Ser Asp Ser Asp Arg Phe Arg Phe Val Arg Gly Asp
50 55 60
Ile Cys Asp Ala Pro Leu Val Asp Asp Leu Leu Ala Val His Asp Gln
65 70 75 80
Val Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Leu Gly
85 90 95
Ala Ala Asp Phe Val Arg Thr Asn Val Thr Gly Thr Gln Thr Leu Leu
100 105 110
Asp Ala Ala Leu Arg Gln Gly Ile Glu Thr Phe Val His Ile Ser Thr
115 120 125
Asp Glu Val Tyr Gly Ser Ile Asp Ala Gly Ser Trp Pro Glu Thr Ala
130 135 140
Pro Val Ser Pro Asn Ser Leu Tyr Ser Ala Ala Lys Ala Ser Ser Asp
145 150 155 160
Leu Val Ala Leu Ala Tyr His Arg Thr His Gly Leu Asp Val Arg Val
165 170 175
Thr Arg Cys Ser Asn Asn Tyr Gly Ser His Gln Phe Pro Glu Lys Val
180 185 190
Ile Pro Leu Phe Val Thr Ser Leu Leu Asp Gly Arg Glu Val Pro Leu
195 200 205
Tyr Gly Asp Gly Thr Asn Val Arg Asp Trp Leu His Val Asp Asp His
210 215 220

D8
Cont

Val Arg Ala Ile Glu Leu Val Arg Thr Gly Gly Arg Ala Gly Glu Val
 225 230 235 240
 Tyr Asn Ile Gly Gly Gly Thr Glu Leu Ser Asn Lys Glu Leu Thr Gln
 245 250 255
 Leu Leu Leu Asp Ala Cys Gly Ala Gly Trp Asp Arg Val Arg Tyr Val
 260 265 270
 Thr Asp Arg Lys Gly His Asp Arg Arg Tyr Ser Val Asp Cys Thr Lys
 275 280 285
 Ile Arg Arg Glu Leu Gly Tyr Arg Pro Ala Arg Glu Phe Gly Asp Ala
 290 295 300
 Leu Ala Glu Thr Val Ala Trp Tyr Arg His His Arg Ala Trp Trp Glu
 305 310 315 320
 Pro Leu Thr Arg Ala Tyr Gly Ala Val Ala Ala
 325 330

<210> 118
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 6-His tag

<400> 118
 His His His His His His
 1 5

<210> 119
 <211> 256
 <212> PRT
 <213> Artificial

<220>
 <223> Computed consensus sequence.
 <400> 1

Met Arg Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Tyr
 1 5 10 15
 Val Arg Ile Leu Gly Pro Ala Val Val Leu Asp Lys Leu Thr Tyr Ala
 20 25 30
 Gly Asn Asn Leu Val Ala Pro Arg Phe Phe Val Arg Gly Asp Ile Asp
 35 40 45
 Val Val Glu Val Met Asp Val Val Val His Phe Ala Ala Glu Ser His
 50 55 60
 Val Asp Arg Ser Ile Ala Phe Val Thr Asn Val Gly Thr Asn Thr Leu
 65 70 75 80

Leu Ala Ala Leu Gly Val Lys Phe Val His Val Ser Thr Asp Glu Val
 85 90 95
 Tyr Gly Ser Ile Gly Ser Trp Pro Glu Asp Pro Leu Pro Asn Ser Pro
 100 105 110
 Tyr Ala Lys Ala Gly Ser Asp Leu Ile Ala Leu Ala Tyr His Arg Thr
 115 120 125
 His Gly Leu Asp Val Val Thr Arg Cys Ser Asn Asn Tyr Gly Pro Gln
 130 135 140
 Phe Pro Glu Lys Val Leu Pro Leu Phe Ile Thr Asn Leu Leu Asp Gly
 145 150 155 160
 Val Pro Leu Tyr Gly Asp Gly Asn Arg Asp Trp Leu His Val Asp His
 165 170 175
 Cys Arg Gly Ile Leu Val Gly Arg Ala Gly Glu Ile Tyr Asn Ile Gly
 180 185 190
 Gly Gly Thr Glu Leu Thr Asn Glu Leu Thr Val Leu Glu Cys Gly Asp
 195 200 205
 Trp Ser Val Val Asp Arg Gly His Asp Arg Arg Tyr Ser Val Asp Thr
 210 215 220
 Lys Ile Arg Glu Leu Gly Tyr Pro Phe Glu Gly Leu Ala Thr Val Trp
 225 230 235 240
 Tyr Arg Asp Asn Arg Ala Trp Trp Glu Leu Pro Leu Lys Ala Gly Gly
 245 250 255

Ser
 E1
 18
 Cont